

**Figure 1:**  
**ATRX open reading frame (SEQ ID NO:1) and translation to corresponding polypeptide (SEQ ID NO:2)**

1	ATG	ACC	GCT	GAG	CCC	ATG	AGT	GAA	AGC	AAG	TTG	AAT	ACA	TTG	GTG	45
1	M	T	A	E	P	M	S	E	S	K	L	N	T	L	V	15
46	CAG	AAG	CTT	CAT	GAC	TTC	CTT	GCA	CAC	TCA	TCA	GAA	GAA	TCT	GAA	90
16	Q	K	L	H	D	F	L	A	H	S	S	E	E	S	E	30
91	GAA	ACA	AGT	TCT	CCT	CCA	CGA	CTT	GCA	ATG	AAT	CAA	AAC	ACA	GAT	135
31	E	T	S	S	P	P	R	L	A	M	N	Q	N	T	D	45
136	AAA	ATC	AGT	GGT	TCT	GGA	AGT	AAC	TCT	GAT	ATG	ATG	GAA	AAC	AGC	180
46	K	I	S	G	S	G	S	N	S	D	M	M	M	E	N	60
181	AAG	GAA	GAG	GGA	ACT	AGC	TCT	TCA	GAA	AAA	TCC	AAG	TCT	TCA	GGA	225
61	K	E	E	G	T	S	S	S	E	K	S	K	S	S	G	75
226	TCG	TCA	CGA	TCA	AAG	AGG	AAA	CCT	TCA	ATT	GTA	ACA	AAG	TAT	GTA	270
76	S	S	R	S	K	R	K	P	S	I	V	T	K	Y	V	90
271	GAA	TCA	GAT	GAT	GAA	AAA	CCT	TTG	GAT	GAT	GAA	ACT	GTA	AAT	GAA	315
91	E	S	D	D	E	K	P	L	D	D	E	T	V	N	E	105
316	GAT	GCG	TCT	AAT	GAA	AAT	TCA	GAA	AAT	GAT	ATT	ACT	ATG	CAG	AGC	360
106	D	A	S	N	E	N	S	E	N	D	I	T	M	Q	S	120
361	TTG	CCA	AAA	GGT	ACA	GTG	ATT	GTA	CAG	CCA	GAG	CCA	GTG	CTG	AAT	405
121	L	P	K	G	T	V	I	V	Q	P	E	P	V	L	N	135
406	GAA	GAC	AAA	GAT	GAT	TTT	AAA	GGG	CCT	GAA	TTT	AGA	AGC	AGA	AGT	450
136	E	D	K	D	D	F	K	G	P	E	F	R	S	R	S	150
451	AAA	ATG	AAA	ACT	GAA	AAT	CTC	AAA	AAA	CCG	GGA	GAA	GAT	GGG	CTT	495
151	K	M	K	T	E	N	L	K	K	R	G	E	D	G	L	165
496	CAT	GGG	ATT	GTG	AGC	TGC	ACT	GCT	TGT	GGA	CAA	CAG	GTC	AAT	CAT	540
166	H	G	I	V	S	C	T	A	C	G	Q	Q	V	N	H	180
541	TTT	CAA	AAA	GAT	TCC	ATT	TAT	AGA	CAC	CCT	TCA	TTG	CAA	GTT	CTT	585
181	F	Q	K	D	S	I	Y	R	H	P	S	L	Q	V	L	195
586	ATT	TGT	AAG	AAT	TGC	TTT	AAG	TAT	TAC	ATG	AGT	GAT	GAT	ATT	AGC	630
196	I	C	K	N	C	F	K	Y	Y	M	S	D	D	I	S	210
631	CGT	GAC	TCA	GAT	GGA	ATG	GAT	GAA	CAA	TGT	AGG	TGG	TGT	GCG	GAA	675
211	R	D	S	D	G	M	D	E	Q	C	R	W	C	A	E	225
676	GGT	GGA	AAC	TTG	ATT	TGT	TGT	GAC	TTT	TGC	CAT	AAT	GCT	TTC	TGC	720
226	G	G	N	L	I	C	C	D	F	C	H	N	A	F	C	240
721	AAG	AAA	TGC	ATT	CTA	CGC	AAC	CTT	GGT	CGA	AAG	GAG	TTG	TCC	ACA	765
241	K	K	C	I	L	R	N	L	G	R	K	E	L	S	T	255
766	ATA	ATG	GAT	GAA	AAC	AAC	CAA	TGG	TAT	TGC	'TAC	ATT	TGT	CAC	CCA	810
256	I	M	D	E	N	N	Q	W	Y	C	Y	I	C	H	P	270
811	GAG	CCT	TTG	TTG	GAC	TTG	GTC	ACT	GCA	TGT	AAC	AGC	GTA	TTT	GAG	855
271	E	P	L	L	D	L	V	T	A	C	N	S	V	F	E	285
856	AAT	TTA	GAA	CAG	TTG	TTG	CAG	CAA	AAT	AAG	AAG	ATA	AAA	GTT		900

286	N	L	E	Q	L	L	Q	Q	N	K	K	K	I	K	V	300
901	GAC	AGT	GAA	AAG	AGT	AAT	AAA	GTA	TAT	GAA	CAT	ACA	TCC	AGA	TTT	945
301	D	S	E	K	S	N	K	V	Y	E	H	T	S	R	F	315
946	TCT	CCA	AAG	AAG	ACT	AGT	TCA	AAT	TGT	AAT	GGA	GAA	GAA	AAG	AAA	990
316	S	P	K	K	T	S	S	N	C	N	G	E	E	K	K	330
991	TTA	GAT	GAT	TCC	TGT	TCT	GGC	TCT	GTA	ACC	'TAC	TCT	TAT	TCC	GCA	1035
331	L	D	D	S	C	S	G	S	V	T	Y	S	Y	S	A	345
1036	CTA	ATT	GTG	CCC	AAA	GAG	ATG	ATT	AAG	AAG	GCA	AAA	AAA	CTG	ATT	1080
346	L	I	V	P	K	E	M	I	K	K	A	K	K	L	I	360
1081	GAG	ACC	ACA	GCC	AAC	ATG	AAC	TCC	AGT	TAT	GTT	AAA	TTT	TTA	AAG	1125
361	E	T	T	A	N	M	N	S	S	Y	V	K	F	L	K	375
1126	CAG	GCA	ACA	GAT	AAT	TCA	GAA	ATC	AGT	TCT	GCT	ACA	AAA	TTA	CGT	1170
376	Q	A	T	D	N	S	E	I	S	S	A	T	K	L	R	390
1171	CAG	CTT	AAG	GCT	TTT	AAG	TCT	GTG	TTG	GCT	GAT	ATT	AAG	AAG	GCT	1215
391	Q	L	K	A	F	K	S	V	L	A	D	I	K	K	A	405
1216	CAT	CTT	GCA	TTG	GAA	GAA	GAC	TTA	AAT	TCC	GAG	TTT	CGA	GCG	ATG	1260
406	H	L	A	L	E	E	D	L	N	S	E	F	R	A	M	420
1261	GAT	GCT	GTA	AAC	AAA	GAG	AAA	AAT	ACC	AAA	GAG	CAT	AAA	GTC	ATA	1305
421	D	A	V	N	K	E	K	N	T	K	E	H	K	V	I	435
1306	GAT	GCT	AAG	TTT	GAA	ACA	AAA	GCA	CGA	AAA	GGA	GAA	AAA	CCT	TGT	1350
436	D	A	K	F	E	T	K	A	R	K	G	E	K	P	C	450
1351	GCT	TTG	GAA	AAG	AAG	GAT	ATT	TCA	AAG	TCA	GAA	GCT	AAA	CTT	TCA	1395
451	A	L	E	K	K	D	I	S	K	S	E	A	K	L	S	465
1396	AGA	AAA	CAG	GTA	GAT	AGT	GAG	CAC	ATG	CAT	CAG	AAT	GTT	CCA	ACA	1440
466	R	K	Q	V	D	S	E	H	M	H	Q	N	V	P	T	480
1441	GAG	GAA	CAA	AGA	ACA	AAT	AAA	AGY	ACC	GGT	GGT	GAA	CAT	AAG	AAA	1485
481	E	E	Q	R	T	N	K	X	T	G	G	E	H	K	K	495
1486	TCT	GAT	AGA	AAA	GAA	GAA	CCT	CAA	TAT	GAA	CCT	GCC	AAC	ACT	TCT	1530
496	S	D	R	K	E	E	P	Q	Y	E	P	A	N	T	S	510
1531	GAA	GAT	TTA	GAC	ATG	GAT	ATT	GTG	TCT	GTT	CCT	TCC	TCA	GTT	CCA	1575
511	E	D	L	D	M	D	I	V	S	V	P	S	S	V	P	525
1576	GAA	GAC	ATT	TTT	GAG	AAT	CTT	GAG	ACT	GCT	ATG	GAA	GTT	CAG	AGT	1620
526	E	D	I	F	E	N	L	E	T	A	M	E	V	Q	S	540
1621	TCA	GTT	GAT	CAT	CAA	GGG	GAT	GGC	AGC	AGT	GGA	ACT	GAA	CAA	GAA	1665
541	S	V	D	H	Q	G	D	G	S	S	G	T	E	Q	E	555
1666	GTG	GAG	AGT	TCA	TCT	GTA	AAA	TTA	AAT	ATT	TCT	TCA	AAA	GAC	AAC	1710
556	V	E	S	S	S	V	K	L	N	I	S	S	K	D	N	570
1711	AGA	GGA	GGT	ATT	AAA	TCA	AAA	ACT	ACA	GCT	AAA	GTA	ACA	AAA	GAA	1755
571	R	G	G	I	K	S	K	T	T	A	K	V	T	K	E	585
1756	TTA	TAT	GTT	AAA	CTC	ACT	CCT	GTT	TCC	CTT	CCT	AAT	TCC	CCA	ATT	1800
586	L	Y	V	K	L	T	P	V	S	L	P	N	S	P	I	600
1801	AAA	GGT	GCT	GAT	TGT	CAG	GAA	GTT	CCA	CAA	GAT	AAA	GAT	GGC	TAT	1845
601	K	G	A	D	C	Q	E	V	P	Q	D	K	D	G	Y	615

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1846	AAA AGT TGT GGT CTG AAC CCC AAG TTA GAG AAA TGT GGA CTT GGA	1890
616	K S C G L N P K L E K C G L G	630
1891	CAG GAA AAC AGT GAT AAT GAG CAT TTG GTT GAA AAT GAA GTT TCA	1935
631	Q E N S D N E H L V E N E V S	645
1936	TTA CTT TTA GAG GAA TCT GAT CTT CGG AGA TCC CCA CGT GTA AAG	1980
646	L L L E E S D L R R S P R V K	660
1981	ACT ACA CCC TTG AGG CGA CCG ACA GAA ACT AAC CCT GTA ACA TCT	2025
661	T T P L R R P T E T N P V T S	675
2026	AAT TCA GAT GAA GAA TGT AAT GAA ACA GTT AAG GAG AAA CAA AAA	2070
676	N S D E E C N E T V K E K Q K	690
2071	CTA TCA GTT CCA GTG AGA AAA AAG GAT AAG CGT AAT TCT TCT GAC	2115
691	L S V P V R K K D K R N S S D	705
2116	AGT GCT ATA GAT AAT CCT AAG CCT AAT AAA TTG CCA AAA TCT AAG	2160
706	S A I D N P K P N K L P K S K	720
2161	CAA TCA GAG ACT GTG GAT CAA AAT TCA GAT TCT GAT GAA ATG CTA	2205
721	Q S E T V D Q N S D S D E M L	735
2206	GCA ATC CTC AAA GGG GTG AGC AGG ATG AGT CAC AGT TCT TCT TCA	2250
736	A I L K G V S R M S H S S S S	750
2251	GAT ACT GAT ATT AAT GAA ATT CAT ACA AAC CAT AAG ACT TTG TAT	2295
751	D T D I N E I H T N H K T L Y	765
2296	GAT TTA AAG ACT CAG GCG GGG AAA GAT GAT AAA GGA AAA AGG AAA	2340
766	D L K T Q A G K D D K G K R K	780
2341	CGA AAA AGT TCT ACA TCT GGC TCA GAT TTT GAT ACT AAA AAG GGC	2385
781	R K S S T S G S D F D T K K G	795
2386	AAA TCA GCT AAG AGC TCT ATA ATT TCT AAA AAG AAA CGA CAA ACC	2430
796	K S A K S S I I S K K R Q T	810
2431	CAG TCT GAG TCT TCT AAT TAT GAC TCA GAA TTA GAA AAA GAG ATA	2475
811	Q S E S S N Y D S E L E K E I	825
2476	AAG AGC ATG AGT AAA ATT GGT GCT GCC AGA ACC ACC AAA AAA AGA	2520
826	K S M S K I G A A R T T K K R	840
2521	ATT CCA AAT ACA AAA GAT TTT GAC TCT TCT GAA GAT GAG AAA CAC	2565
841	I P N T K D F D S S E D E K H	855
2566	AGC AAA AAA GGA ATG GAT AAT CAA GGG CAC AAA AAT TTG AAG ACC	2610
856	S K K G M D N Q G H K N L K T	870
2611	TCA CAA GAA GGA TCA TCT GAT GAT GCT GAA AGA AAA CAA GAG AGA	2655
871	S Q E G S S D D A E R K Q E R	885
2656	GAG ACT TTC TCT TCA GCA GAA GGC ACA GTT GAT AAA GAC ACG ACC	2700
886	E T F S S A E G T V D K D T T	900
2701	ATC ATG GAA TTA AGA GAT CGA CTT CCT AAG AAG CAG CAA GCA AGT	2745
901	I M E L R D R L P K K Q Q A S	915
2746	GCT TCC ACT GAT GGT GTC GAT AAG CTT TCT GGG AAA GAG CAG AGT	2790
916	A S T D G V D K L S G K E Q S	930
2791	TTT ACT TCT TTG GAA GTT AGA AAA GTT GCT GAA ACT AAA GAA AAG	2835
931	F T S L E V R K V A E T K E K	945

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2836	AGC AAG CAT CTC AAA ACC AAA ACA TGT AAA AAA GTA CAG GAT GGC	2880
946	S K H L K T K T C K K V Q D G	960
2881	TTA TCT GAT ATT GCA GAG AAA TTC CTA AAG AAA GAC CAG AGC GAT	2925
961	L S D I A E K F L K K D Q S D	975
2926	GAA ACT TCT GAA GAT GAT AAA AAG CAG AGC AAA AAG GGA ACT GAA	2970
976	E T S E D D K K Q S K K G T E	990
2971	GAA AAA AAG AAA CCT TCA GAC TTT AAG AAA AAA GTA ATT AAA ATG	3015
991	E K K K P S D F K K K V I K M	1005
3016	GAA CAA CAG TAT GAA TCT TCA TCT GAT GGC ACT GAA AAG TTA CCT	3060
1006	E Q Q Y E S S S D G T E K L P	1020
3061	GAG CGA GAA GAA ATT TGT CAT TTT CCT AAG GGC ATA AAA CAA ATT	3105
1021	E R E E I C H F P K G I K Q I	1035
3106	AAG AAT GGA ACA ACT GAT GGA GAA AAG AAA AGT AAA AAA ATA AGA	3150
1036	K N G T T D G E K K S K K I R	1050
3151	GAT AAA ACT TCT AAA AAG AAG GAT GAA TTA TCT GAT TAT GCT GAG	3195
1051	D K T S K K K D E L S D Y A E	1065
3196	AAG TCA ACA GGG AAA GGA GAT AGT TGT GAC TCT TCA GAG GAT AAA	3240
1066	K S T G K G D S C D S S E D K	1080
3241	AAG AGT AAG AAT GGA GCA TAT GGT AGA GAG AAG AAA AGG TGC AAG	3285
1081	K S K N G A Y G R E K K R C K	1095
3286	TTG CTT GGA AAG AGT TCA AGG AAG AGA CAA GAT TGC TCA TCA TCT	3330
1096	L L G K S S R K R Q D C S S S	1110
3331	GAT ACT GAG AAA TAT TCC ATG AAA GAA GAT GGT TGT AAC TCT TCT	3375
1111	D T E K Y S M K E D G C N S S	1125
3376	GAT AAG AGA CTG AAA AGA ATA GAA TTG AGG GAA AGA AGA AAT TTA	3420
1126	D K R L K R I E L R E R R N L	1140
3421	AGT TCA AAG AGA AAT ACT AAG GAA ATA CAA AGT GGC TCA TCA TCA	3465
1141	S S K R N T K E I Q S G S S S	1155
3466	TCT GAT GCT GAG GAA AGT TCT GAA GAT AAT AAA AAG AAG AAG CAA	3510
1156	S D A E E S S E D N K K K K Q	1170
3511	AGA ACT TCA TCT AAA AAG AAG GCA GTC ATT GTC AAG GAG AAA AAG	3555
1171	R T S S K K K A V I V K E K K	1185
3556	AGA AAC TCC CTA AGA ACA AGC ACT AAA AGG AAG CAA GCT GAC ATT	3600
1186	R N S L R T S T K R K Q A D I	1200
3601	ACA TCC TCA TCT TCT GAT ATA GAA GAT GAT GAT CAG AAT TCT	3645
1201	T S S S S D I E D D D Q N S	1215
3646	ATA GGT GAG GGA AGC AGC GAT GAA CAG AAA ATT AAG CCT GTC ACT	3690
1216	I G E G S S D E Q K I K P V T	1230
3691	GAA AAT TTA GTG CTG TCT TCA CAT ACT GGA TTT TGC CAA TCT TCA	3735
1231	E N L V L S S H T G F C Q S S	1245
3736	GGA GAT GAA GCC TTA TCT AAA TCA GTG CCT GTC ACA GTG GAT GAT	3780
1246	G D E A L S K S V P V T V D D	1260
3781	GAT GAT GAC GAC AAT GAT CCT GAG AAT AGA ATT GCC AAG AAG ATG	3825

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1261	D	D	D	D	N	D	P	E	N	R	I	A	K	K	M	1275
3826	CTT	TTA	GAA	GAA	ATT	AAA	GCC	AAT	CTT	TCC	TCT	GAT	GAG	GAT	GGA	3870
1276	L	L	E	E	I	K	A	N	L	S	S	D	E	D	G	1290
3871	TCT	TCA	GAT	GAT	GAG	CCA	GAA	GAA	GGG	AAA	AAA	AGA	ACT	GGA	AAA	3915
1291	S	S	D	D	E	P	E	E	G	K	K	R	T	G	K	1305
3916	CAA	AAT	GAA	GAA	AAC	CCA	GGA	GAT	GAG	GAA	GCA	AAA	AAT	CAA	GTC	3960
1306	Q	N	E	E	N	P	G	D	E	E	A	K	N	Q	V	1320
3961	AAT	TCT	GAA	TCA	GAT	TCA	GAT	TCT	GAA	GAA	TCT	AAG	AAG	CCA	AGA	4005
1321	N	S	E	S	D	S	D	S	E	E	S	K	K	P	R	1335
4006	TAC	AGA	CAT	AGG	CTT	TTG	CGG	CAC	AAA	TTG	ACT	GTG	AGT	GAC	GGA	4050
1336	Y	R	H	R	L	L	R	H	K	L	T	V	S	D	G	1350
4051	GAA	TCT	GGA	GAA	GAA	AAA	AAG	ACA	AAG	CCT	AAA	GAG	CAT	AAA	GAA	4095
1351	E	S	G	E	E	K	K	T	K	P	K	E	H	K	E	1365
4096	GTC	AAA	GGC	AGA	AAC	AGA	AGA	AAG	GTG	AGC	AGT	GAA	GAT	TCA	GAA	4140
1366	V	K	G	R	N	R	R	K	V	S	S	E	D	S	E	1380
4141	GAT	TCT	GAT	TTT	CAG	GAA	TCA	GGA	GTT	AGT	GAA	GAA	GTT	AGT	GAA	4185
1381	D	S	D	F	Q	E	S	G	V	S	E	E	V	S	E	1395
4186	TCC	GAA	GAT	GAA	CAG	CGG	CCC	AGA	ACA	AGG	TCT	GCA	AAG	AAA	GCA	4230
1396	S	E	D	E	Q	R	P	R	T	R	S	A	K	K	A	1410
4231	GAG	TTG	GAA	GAA	AAT	CAG	CGG	AGC	TAT	AAA	CAG	AAA	AAG	AAA	AGG	4275
1411	E	L	E	E	N	Q	R	S	Y	K	Q	K	K	K	R	1425
4276	CGA	CGT	ATT	AAG	GTT	CAA	GAA	GAT	TCA	TCC	AGT	GAA	AAC	AAG	AGT	4320
1426	R	R	I	K	V	Q	E	D	S	S	S	E	N	K	S	1440
4321	AAT	TCT	GAG	GAA	GAA	GAG	GAG	GAA	AAA	GAA	GAG	GAG	GAG	GAA	GAG	4365
1441	N	S	E	E	E	E	E	E	K	E	E	E	E	E	E	1455
4366	GAG	GAG	GAG	GAG	GAA	GAG	GAG	GAG	GAA	GAT	GAA	AAT	GAT	GAT	TCC	4410
1456	E	E	E	E	E	E	E	E	E	D	E	N	D	D	S	1470
4411	AAG	TCT	CCT	GGA	AAA	GGC	AGA	AAG	AAA	ATT	CGG	AAG	ATT	CTT	AAA	4455
1471	K	S	P	G	K	G	R	K	K	I	R	K	I	L	K	1485
4456	GAT	GAT	AAA	CTG	AGA	ACA	GAA	ACA	CAA	AAT	GCT	CTT	AAG	GAA	GAG	4500
1486	D	D	K	L	R	T	E	T	Q	N	A	L	K	E	E	1500
4501	GAA	GAG	AGA	CGA	AAA	CGT	ATT	GCT	GAG	AGG	GAG	CGT	GAG	CGA	GAA	4545
1501	E	E	R	R	K	R	I	A	E	R	E	R	E	R	E	1515
4546	AAA	TTG	AGA	GAG	GTG	ATA	GAA	ATT	GAA	GAT	GCT	TCA	CCC	ACC	AAG	4590
1516	K	L	R	E	V	I	E	I	E	D	A	S	P	T	K	1530
4591	TGT	CCA	ATA	ACA	ACC	AAG	TTG	GTT	TTA	GAT	GAA	GAT	GAA	GAA	ACC	4635
1531	C	P	I	T	T	K	L	V	L	D	E	D	E	E	T	1545
4636	AAA	GAA	CCT	TTA	GTG	CAG	GTT	CAT	AGA	AAT	ATG	GTT	ATC	AAA	TTG	4680
1546	K	E	P	L	V	Q	V	H	R	N	M	V	I	K	L	1560
4681	AAA	CCC	CAT	CAA	GTA	GAT	GGT	GTT	CAG	TTT	ATG	TGG	GAT	TGC	TGC	4725
1561	K	P	H	Q	V	D	G	V	Q	F	M	W	D	C	C	1575
4726	TGT	GAG	TCT	GTG	AAA	AAA	ACA	AAG	AAA	TCT	CCA	GGT	TCA	GGA	TGC	4770
1576	C	E	S	V	K	K	T	K	K	S	P	G	S	G	C	1590

4771	ATT CTT GCC CAC TGT ATG GGC CTT GGT AAG ACT TTA CAG GTG GTA	4815
1591	I L A H C M G L G K T L Q V V	1605
4816	AGT TTT CTT CAT ACA GTT CTT TTG TGT GAC AAA CTG GAT TTC AGC	4860
1606	S F L H T V L L C D K L D F S	1620
4861	ACG GCG TTA GTG GTT TGT CCT CTT AAT ACT GCT TTG AAT TGG ATG	4905
1621	T A L V V C P L N T A L N W M	1635
4906	AAT GAA TTT GAG AAG TGG CAA GAG GGA TTA AAA GAT GAT GAG AAG	4950
1636	N E F E K W Q E G L K D D E K	1650
4951	CTT GAG GTT TCT GAA TTA GCA ACT GTG AAA CGT CCT CAG GAG AGA	4995
1651	L E V S E L A T V K R P Q E R	1665
4996	AGC TAC ATG CTG CAG AGG TGG CAA GAA GAT GGT GGT GTT ATG ATC	5040
1666	S Y M L Q R W Q E D G G V M I	1680
5041	ATA GGC TAT GAG ATG TAT AGA AAT CTT GCT CAA GGA AGG AAT GTG	5085
1681	I G Y E M Y R N L A Q G R N V	1695
5086	AAG AGT CGG AAA CTT AAA GAA ATA TTT AAC AAA GCT TTG GTT GAT	5130
1696	K S R K L K E I F N K A L V D	1710
5131	CCA GGC CCT GAT TTT GTT GTT TGT GAT GAA GGC CAT ATT CTA AAA	5175
1711	P G P D F V V C D E G H I L K	1725
5176	AAT GAA GCA TCT GCT GTT TCT AAA GCT ATG AAT TCT ATA CGA TCA	5220
1726	N E A S A V S K A M N S I R S	1740
5221	AGG AGG AGG ATT ATT TTA ACA GGA ACA CCA CTT CAA AAT AAC CTA	5265
1741	R R R I I L T G T P L Q N N L	1755
5266	ATT GAG TAT CAT TGT ATG GTT AAT TTT ATC AAG GAA AAT TTA CTT	5310
1756	I E Y H C M V N F I K E N L L	1770
5311	GGA TCC ATT AAG GAG TTC AGG AAT AGA TTT ATA AAT CCA ATT CAA	5355
1771	G S I K E F R N R F I N P I Q	1785
5356	AAT GGT CAG TGT GCA GAT TCT ACC ATG GTA GAT GTC AGA GTG ATG	5400
1786	N G Q C A D S T M V D V R V M	1800
5401	AAA AAA CGT GCT CAC ATT CTC TAT GAG ATG TTA GCT GGA TGT GTT	5445
1801	K K R A H I L Y E M L A G C V	1815
5446	CAG AGG AAA GAT TAT ACA GCA TTA ACA AAA TTC TTG CCT CCA AAA	5490
1816	Q R K D Y T A L T K F L P P K	1830
5491	CAC GAA TAT GTG TTA GCT GTG AGA ATG ACT TCT ATT CAG TGC AAG	5535
1831	H E Y V L A V R M T S I Q C K	1845
5536	CTC TAT CAG TAC TAC TTA GAT CAC TTA ACA GGT GTG GGC AAT AAT	5580
1846	L Y Q Y Y L D H L T G V G N N	1860
5581	AGT GAA GGT GGA AGA GGA AAG GCA GGT GCA AAG CTT TTC CAA GAT	5625
1861	S E G G R G K A G A K L F Q D	1875
5626	TTT CAG ATG TTA AGT AGA ATA TGG ACT CAT CCT TGG TGT TTG CAG	5670
1876	F Q M L S R I W T H P W C L Q	1890
5671	CTA GAC TAC ATT AGC AAA GAA AAT AAG GGT TAT TTT GAT GAA GAC	5715
1891	L D Y I S K E N K G Y F D E D	1905
5716	AGT ATG GAT GAA TTT ATA GCC TCA GAT TCT *GAT GAA ACC TCC ATG	5760
1906	S M D E F I A S D S D E T S M	1920

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5761	AGT TTA AGC TCC GAT GAT TAT ACA AAA AAG AAG AAA AAA GGG AAA	5805
1921	S L S S D D Y T K K K K K G K	1935
5806	AAG GGG AAA AAA GAT AGT AGC TCA AGT GGA AGT GGC AGT GAC AAT	5850
1936	K G K K D S S S S G S G S D N	1950
5851	GAT GTT GAA GTG ATT AAG GTC TGG AAT TCA AGA TCT CGG GGA GGT	5895
1951	D V E V I K V W N S R S R G G	1965
5896	GGT GAA GGA AAT GTG GAT GAA ACA GGA AAC AAT CCT TCT GTT TCT	5940
1966	G E G N V D E T G N N P S V S	1980
5941	TTA AAA CTG GAA GAA AGT AAA GCT ACT TCT TCT TCT AAT CCA AGC	5985
1981	L K L E E S K A T S S S N P S	1995
5986	AGC CCA GCT CCA GAC TGG TAC AAA GAT TTT GTT ACA GAT GCT GAT	6030
1996	S P A P D W Y K D F V T D A D	2010
6031	GCT GAG GTT TTA GAG CAT TCT GGG AAA ATG GTA CTT CTC TTT GAA	6075
2011	A E V L E H S G K M V L L F E	2025
6076	ATT CTT CGA ATG GCA GAG GAA ATT GGG GAT AAA GTC CTT GTT TTC	6120
2026	I L R M A E E I G D K V L V F	2040
6121	AGC CAG TCC CTC ATA TCT CTG GAC TTG ATT GAA GAT TTT CTT GAA	6165
2041	S Q S L I S L D L I E D F L E	2055
6166	TTA GCT AGT AGG GAG AAG ACA GAA GAT AAA GAT AAA CCC CTT ATT	6210
2056	L A S R E K T E D K D K P L I	2070
6211	TAT AAA GGT GAG GGG AAG TGG CTT CGA AAC ATT GAC TAT TAC CGT	6255
2071	Y K G E G K W L R N I D Y Y R	2085
6256	TTA GAT GGT TCC ACT ACT GCA CAG TCA AGG AAG AAG TGG GCT GAA	6300
2086	L D G S T T A Q S R K K W A E	2100
6301	GAA TTT AAT GAT GAA ACT AAT GTG AGA GGA CGA TTA TTT ATC ATT	6345
2101	E F N D E T N V R G R L F I I	2115
6346	TCT ACT AAA GCA GGA TCT CTA GGA ATT AAT CTG GTA GCT GCT AAT	6390
2116	S T K A G S L G I N L V A A N	2130
6391	CGA GTA ATT ATA TTC GAC GCT TCT TGG AAT CCA TCT TAT GAC ATC	6435
2131	R V I I F D A S W N P S Y D I	2145
6436	CAG AGT ATA TTC AGA GTT TAT CGC TTT GGA CAA ACT AAG CCT GTT	6480
2146	Q S I F R V Y R F G Q T K P V	2160
6481	TAT GTA TAT AGG TTC TTA GCT CAG GGA ACC ATG GAA GAT AAG ATT	6525
2161	Y V Y R F L A Q G T M E D K I	2175
6526	TAT GAT CGG CAA GTA ACT AAG CAG TCA CTG TCT TTT CGA GTT GTT	6570
2176	Y D R Q V T K Q S L S F R V V	2190
6571	GAT CAG CAG CAG GTG GAG CGT CAT TTT ACT ATG AAT GAG CTT ACT	6615
2191	D Q Q Q V E R H F T M N E L T	2205
6616	GAA CTT TAT ACT TTT GAG CCA GAC TTA TTA GAT GAC CCT AAT TCA	6660
2206	E L Y T F E P D L L D D P N S	2220
6661	GAA AAG AAG AAG AAG AGG GAT ACT CCC ATG CTG CCA AAG GAT ACC	6705
2221	E K K K K R D T P M L P K D T	2235
6706	ATA CTT GCA GAG CTC CTT CAG ATA CAT AAA GAA CAC ATT GTA GGA	6750

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2236	I	L	A	E	L	L	Q	I	H	K	E	H	H	I	V	G	2250
6751	TAC	CAT	GAA	CAT	GAT	TCT	CTT	TTG	GAC	CAC	AAA	GAA	GAA	GAA	GAG	6795	
2251	Y	H	E	H	D	S	L	L	D	H	K	E	E	E	E	2265	
6796	TTG	ACT	GAA	GAA	GAA	AGA	AAA	GCA	GCT	TGG	GCT	GAG	TAT	GAA	GCA	6840	
2266	L	T	E	E	E	R	K	A	A	W	A	E	Y	E	A	2280	
6841	GAG	AAG	AAG	GTA	CTG	ACC	ATG	CGT	TTC	AAC	ATA	CCA	ACT	GGG	ACC	6885	
2281	E	K	K	V	L	T	M	R	F	N	I	P	T	G	T	2295	
6886	AAT	TTA	CCC	CCT	GTC	AGT	TTC	AAC	TCT	CAA	ACT	CCT	TAT	ATT	CCT	6930	
2296	N	L	P	P	V	S	F	N	S	Q	T	P	Y	I	P	2310	
6931	TTC	AAT	TTG	GGA	GCC	CTG	TCA	GCA	ATG	AGT	AAT	CAA	CAG	CTG	GAG	6975	
2311	F	N	L	G	A	L	S	A	M	S	N	Q	Q	L	E	2325	
6976	GAC	CTC	ATT	AAT	CAA	GGA	AGA	GAA	AAA	GTT	GTA	GAA	GCA	ACA	AAC	7020	
2326	D	L	I	N	Q	G	R	E	K	V	V	E	A	T	N	2340	
7021	AGT	GTG	ACA	GCA	GTG	AGG	ATT	CAA	CCT	CTT	GAG	GAT	ATA	ATT	TCA	7065	
2341	S	V	T	A	V	R	I	Q	P	L	E	D	I	I	S	2355	
7066	GCT	GTA	TGG	AAG	GAG	AAC	ATG	AAT	CTC	TCA	GAG	GCC	CAA	GTA	CAG	7110	
2356	A	V	W	K	E	N	M	N	L	S	E	A	Q	V	Q	2370	
7111	GCG	TTA	GCA	TTA	AGT	AGA	CAA	GCC	AGC	CAG	GAG	CTT	GAT	GTT	AAA	7155	
2371	A	L	A	L	S	R	Q	A	S	Q	E	L	D	V	K	2385	
7156	CGA	AGA	GAA	GCA	ATC	TAC	AAT	GAT	GTA	TTG	ACA	AAA	CAA	CAG	ATG	7200	
2386	R	R	E	A	I	Y	N	D	V	L	T	K	Q	Q	M	2400	
7201	TTA	ATC	AGC	TGT	GTT	CAG	CGA	ATA	CTT	ATG	AAC	AGA	AGG	CTC	CAG	7245	
2401	L	I	S	C	V	Q	R	I	L	M	N	R	R	L	Q	2415	
7246	CAG	CAG	TAC	AAT	CAG	CAG	CAA	CAG	CAA	CAA	ATG	ACT	TAT	CAA	CAA	7290	
2416	Q	Q	Y	N	Q	Q	Q	Q	Q	Q	M	T	Y	Q	Q	2430	
7291	GCA	ACA	CTG	GGT	CAC	CTC	ATG	ATG	CCA	AAG	CCC	CCA	AAT	TTG	ATC	7335	
2431	A	T	L	G	H	L	M	M	P	K	P	P	N	L	I	2445	
7336	ATG	AAT	CCT	TCT	AAC	TAC	CAG	CAG	ATT	GAT	ATG	AGA	GGA	ATG	TAT	7380	
2446	M	N	P	S	N	Y	Q	Q	I	D	M	R	G	M	Y	2460	
7381	CAG	CCA	GTG	GCT	GGT	GGT	ATG	CAG	CCA	CCA	CCA	TTA	CAG	CGT	GCA	7425	
2461	Q	P	V	A	G	G	M	Q	P	P	P	L	Q	R	A	2475	
7426	CCA	CCC	CCA	ATG	AGA	AGC	AAA	AAT	CCA	GGA	CCT	TCC	CAA	GGG	AAA	7470	
2476	P	P	P	M	R	S	K	N	P	G	P	S	Q	G	K	2490	
7471	TCA	ATG	TGA													7479	
2491	S	M	*														

**Figure 2:**  
**ATRX Antisense fragments**

**Fragment No. 1: HAP\_66D4 (SEQ ID NO:3)**

5' TGCACCTGCCTTCCCTTCCACCTTCACTATTATTGCCACACCTGTTAAGTGATCTAAGT  
AGTACTGATAGAGCTTGCCTGAATAGAACAGTCATTCTCACAGCTAACACATATTGTGTTGG  
AGGCAAGAATTGGTTAATGCTGTATAATCTTCCCTGAACACATCCAGCTAACATCTCATAG  
AGAATGTGAGCAGCTTTTCATCACTCTGACATCTACCATGGTAGAATCTGCACACTGACCAT  
TTTGAATTGGATTATAAACTATTCTGAACCTTAAT 3'

**Fragment No. 2: TXA\_1B3 (SEQ ID NO:4)**

5' GCTTAGTGCAAATACATTGATTCCCTGGAAAGGTCCCTGGATTTGCTTCTCATTGGGG  
GTGGTGACGCTGTAATGGTGGCTGCATACCAACCAGCCACTGGCTGATACATTCCCTCAT  
ATCAATCTGCTGGTAGTTAGAAGGATTGATCAAATTGGGGCTTGGCATCATGAGGTGA  
CCCAGTGTGCTTGTGATAAGTCATTGTTGCTGCTGATGATTGACTGCTGCTGGAGCC  
TTCTGTTCATAGTATTGCTGAACACAGCTGATTAACATCT 3'

**Figure 3:**  
**Alignment between the ATRX open reading frame and the corresponding sense polynucleotide of the ATRX Antisense Fragments**

**a) AS Fragment No. 1 (HAP-66D4)**

ATRX ORF	1	ATGACCGCTGAGCCCATGAGTGAAGCAAGTTGAATACATTGGTCAGAAGCTTCATGACTTCCTGCACACTCATCAGA
HAP-66D4	1	-----
ATRX ORF	81	AGAACTGAAGAACAAAGTTCTCCACGACTTCAATGAATCAAACACAGATAAAATCAGTGGTCTGGAAGTAAC
HAP-66D4	1	-----
ATRX ORF	161	CTGATATGATGGAAAACAGCAAGGAAGAGGGAACTAGCTCTCAGAAAAATCCAAGTCTCAGGATCGTCACGATCAAAG
HAP-66D4	1	-----
ATRX ORF	241	AGGAAACCTTCATTGTAACAAAGTATGTAGAATCAGATGATGAAAAACCTTGGATGATGAAACTGTAAATGAAGATGC
HAP-66D4	1	-----
ATRX ORF	321	GTCTAATGAAAATTCAAGAAAATGATATTACTATGCAGAGCTGCCAAAGGTACAGTGATTGTACAGCCAGAGCCAGTGC
HAP-66D4	1	-----
ATRX ORF	401	TGAATGAAGACAAAGATGATTTAAAGGGCTGAATTAGAAGCAGAAGTAAAATGAAAATCTCAAAAAACGC
HAP-66D4	1	-----
ATRX ORF	481	GGAGAAGATGGGCTTCATGGGATTGTGAGCTGCACTGCTTGGACAACAGGTCAATCTTCAAAAAGATTCCATTAA
HAP-66D4	1	-----
ATRX ORF	561	TAGACACCCTTCATTGCAAGTTCTTATTGTAAGAATTGCTTAAGTATTACATGAGTGATGATATTAGCCGTGACTCAG
HAP-66D4	1	-----
ATRX ORF	641	ATGGAATGGATGAAACATGTAGGTGGTGTGCGGAAGGTGAAACTTGATTGTTGTGACTTTGCCATAATGCTTCATG
HAP-66D4	1	-----
ATRX ORF	721	AAGAAAATGCATTCTACGCAACCTTGGTCGAAGGGAGTTGTCCACAATAATGGATGAAAACAACCAATGGTATTGCTACAT
HAP-66D4	1	-----
ATRX ORF	801	TTGTCACCCAGAGCCTTGTGGACTTGGTCACTGCATGTAACAGCGTATTGAGAATTAGAACAGTTGTTGCAGCAAA
HAP-66D4	1	-----
ATRX ORF	881	ATAAGAAGAAGATAAAAGTTGACAGTGAAAGAGTAATAAGTATATGAACATACATCCAGATTCTCCAAAGAAGACT
HAP-66D4	1	-----
ATRX ORF	961	AGTTCAAATTGTAATGGAGAAGAAAAGAAATTAGATGATTCTGTCTGGCTCTGTAACCTACTCTTATTCCGCACTAAT
HAP-66D4	1	-----
ATRX ORF	1041	TGTGCCAAAGAGATGATTAAGAAGGCCAAAAACTGATTGAGACCACAGCCAACATGAACCTCCAGTTATGTTAAATT
HAP-66D4	1	-----
ATRX ORF	1121	TAAAGCAGGCAACAGATAATTCAAGAAATCAGTCTGCTACAAAATTACGTCAAGCTTAAGGCTTTAAGTCTGTGTTGGCT
HAP-66D4	1	-----
ATRX ORF	1201	GATATTAAGAAGGCTCATCTGCATTGGAAGAAGACTTAAATTCCGAGTTCGAGCGATGGATGCTGAAACAAAGAGAA
HAP-66D4	1	-----
ATRX ORF	1281	AAATACCAAGAGCATAAAAGTCATAGATGCTAAGTTGAAACAAAAGCACGAAAAGGAGAAAACCTTGTGCTTGGAAA
HAP-66D4	1	-----
ATRX ORF	1361	AGAAGGATATTCAGAACAGCTAAACTTCAAGAAAACAGGTAGATAGTGAGCAGTCATGCAATGTTCCAAACA
HAP-66D4	1	-----
ATRX ORF	1441	GAGGAACAAAGAACAAATAAAAGYACCGGTGGTGAACATAAGAAAATCTGATAGAAAAGAAGAACCTCAATATGAACCTGC
HAP-66D4	1	-----
ATRX ORF	1521	CAACACTTCTGAAGATTAGACATGGATATTGTGCTGTTCTTCAGTTCCAGAAGACATTGAGAATCTTGTGAGA
HAP-66D4	1	-----
ATRX ORF	1601	CTGCTATGGAAGTTCAGAGTTCAAGTGTGATCATCAAGGGATGGCAGCAGTGGAACTGAACAAAGTGGAGAGTTCATCT
HAP-66D4	1	-----
ATRX ORF	1681	GTAAAATTAAATATTCTCAAAAGACAACAGAGGAGGTATTAATCAAAAACAGCTAAAGTAACAAAAGAATTATA

HAP-66D4	1	-----
ATRX ORF	1761	TGTTAAACTCACTCCTGTTCCCTCTAATCCCCAATTAAAGGTGCTGATTGTCAGGAAGTTCCACAAGATAAAGATG-----
HAP-66D4	1	-----
ATRX ORF	1841	GCTATAAAAGTTGGTCTGAACCCCAAGTTAGAGAAATGTTGACTTGACAGGAAAACAGTGATAATGAGCATTGGTT-----
HAP-66D4	1	-----
ATRX ORF	1921	GAAAATGAAGTTCTTACAGTTAGAGGAATCTGATCTCGAGATCCCACGTGTAAAGACTACACCCCTGAGGCAGCC-----
HAP-66D4	1	-----
ATRX ORF	2001	GACAGAAAACAACCCCTGTAACATCTAATTCACTGAGAAGAATGTAATGAAACAGTTAAGGAGAAAACAAAATCATCAGTTC-----
HAP-66D4	1	-----
ATRX ORF	2081	CAGTGAGAAAAAGGATAAGCGTAATTCTCTGACAGTGCTATAGATAATCTAACGCCTAATAAATTGCCAAAATCTAAG-----
HAP-66D4	1	-----
ATRX ORF	2161	CAATCAGAGACTGTGGATCAAAATTCACTGAGATTCTGATGAAATGCTAGCAATCCTCAAAGGGTGAGCAGGATGAGTCACAG-----
HAP-66D4	1	-----
ATRX ORF	2241	TTCTTCTTCAGATACTGATATTAAATGAAATTCAACAAACCATAAAGACTTGTATGATTTAAAGACTCAGGCGGGGAAAG-----
HAP-66D4	1	-----
ATRX ORF	2321	ATGATAAAGGAAAAAGGAAACGAAAAAGTTCTACATCTGGCTCAGATTTGATACTAAAAAGGGCAAATCAGCTAACAGC-----
HAP-66D4	1	-----
ATRX ORF	2401	TCTATAATTCTAAAAAGAACGACAACCCACTGAGTCTCTAATTGACTCAGAATTAGAAAAAGAGATAAAGAG-----
HAP-66D4	1	-----
ATRX ORF	2481	CATGAGTAAAATTGGTCTGCCAGAACCAACCAAAAAAGAATTCCAATACAAAAGATTGACTCTCTGAAGATGAGA-----
HAP-66D4	1	-----
ATRX ORF	2561	AACACAGCAAAAAGGAATGGATAATCAAGGGCACAAAATTGAAGACCTCACAGAACGGATCATCTGATGATGCTGAA-----
HAP-66D4	1	-----
ATRX ORF	2641	AGAAAACAAGAGAGAGAGACTTCTCTCAGCAGAACGGCACAGTTGATAAAAGACACGACCACATGGAATTAGAGATCG-----
HAP-66D4	1	-----
ATRX ORF	2721	ACTTCCTAACAGCAGCAAGCAAGTGCTTCACTGATGGTGTGATAAGCTTCTGGAAAGAGCAGAGTTTACTTCT-----
HAP-66D4	1	-----
ATRX ORF	2801	TGGAAGTTAGAAAAGTTGCTGAAACTAAAGAAAAGAGCAAGCATCTCAAAACAAAACATGAAAAAGTACAGGATGGC-----
HAP-66D4	1	-----
ATRX ORF	2881	TTATCTGATATTGCAGAGAAAATTCTAAAGAAAGACCAGAGCGATGAAACTCTGAAAGATGATAAAAGCAGAGCAAAA-----
HAP-66D4	1	-----
ATRX ORF	2961	GGGAACCTGAAAGAAAAAGAACCTCAGACTTAAGAAAAAGTAATTAAATGGAACAAACAGTATGAAATCTCATCTG-----
HAP-66D4	1	-----
ATRX ORF	3041	ATGGCACTGAAAAGTTACCTGAGCGAGAAGAAATTGTCATTCTAACGGCATAAAACAAATTAGAATGGAACAACACT-----
HAP-66D4	1	-----
ATRX ORF	3121	GATGGAGAAAAGAAAAGTAAAAAATAAGAGATAAAACTCTAAAGAACGGATTAAGTCTGATTATGCTGAGAAGTC-----
HAP-66D4	1	-----
ATRX ORF	3201	AACAGGGAAAGGAGATAGTTGACTCTCAGAGGATAAAAGAGTAAGAACGGCATATGGTAGAGAGAAGAAAAGGT-----
HAP-66D4	1	-----
ATRX ORF	3281	GCAAGTTGCTTGGAAAGAGTTCAAGGAAGAGACAAGATTGCTCATCTGATACTGAGAAATTCCATGAAAGAAGAT-----
HAP-66D4	1	-----
ATRX ORF	3361	GGTTGTAACCTCTGATAAGAGACTGAAAAGAAATAGAATTGAGGGAAAGAAGAAATTAAAGTTCAAAAGAGAAATCTAA-----
HAP-66D4	1	-----
ATRX ORF	3441	GGAAATACAAAGTGGCTCATCATCTGATGCTGAGGAAAGTTCTGAAAGATAATAAAAGAAGAACGAAACTTCAT-----
HAP-66D4	1	-----
ATRX ORF	3521	CTAAAAAGAAGGCAGTCATTGTCAGGGAGAAAAGAGAAAACCTCTAACAGAACAGCAACTAAAGGAAGCAAGCTGACATT-----
HAP-66D4	1	-----
ATRX ORF	3601	ACATCCTCATCTCTGATATAGAAGATGATGATCAGAATTCTATAGGTGAGGGAAAGCAGCGATGAAACAGAAAATTAA-----
HAP-66D4	1	-----

ATRX ORF HAP-66D4	3681	GCCTGTCACTGAAAATTAGTGTCTTCACATACTGGATTTGCCAATCTCAGGAGATGAAGCCTATCTAAATCAG
	1	-----
ATRX ORF HAP-66D4	3761	TGCCCTCACAGTGGATGATGATGACGACAATGATCCTGAGAATAGAATTGCCAAGAAGATGCTTTAGAAGAAATT
	1	-----
ATRX ORF HAP-66D4	3841	AAAGCCAATCTTCCTCTGATGAGGATGGATCTCAGATGATGAGGCCAGAAGAAGGGAAAAAGAACTGGAAAACAAAA
	1	-----
ATRX ORF HAP-66D4	3921	TGAAGAAAACCAGGAGATGAGGAAGCAAAAATCAAGTCATTCTGAATCAGATTCTGAAGAATCTAAGAAC
	1	-----
ATRX ORF HAP-66D4	4001	CAAGATAACAGACATAGGCTTTGCGGCACAAATTGACTGTGAGTGACGGAGAATCTGGAGAAGAAAAAGACAAAGCCT
	1	-----
ATRX ORF HAP-66D4	4081	AAAGAGCATAAAGAAGTCAAAGGCAGAACAGAAAGAAAGGTGAGCAGTGAAGATTCTGAGATTCTGAGGAAATC
	1	-----
ATRX ORF HAP-66D4	4161	AGGAGTTAGTGAAGAAGTTAGTGAATCCGAAGATGAACAGCGGCCAGAACAAAGGTCTGCAAAGAAAGCAGAGTTGGAAG
	1	-----
ATRX ORF HAP-66D4	4241	AAAATCAGCGGAGCTATAAACAGAAAAGAAAAGGCACGTATTAAGGTTCAAGAAGATTCACTCCAGTGAAAACAAGAGT
	1	-----
ATRX ORF HAP-66D4	4321	AATTCTGAGGAAGAAGAGGAGGAAAAGAAGAGGAGGAGGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGATGAAA
	1	-----
ATRX ORF HAP-66D4	4401	TGATGATTCCAAGTCTCCTGGAAAAGGCAGAAAGAAAATTCGGAAGATTCTTAAAGATGATAAACTGAGAACAGAACAC
	1	-----
ATRX ORF HAP-66D4	4481	AAAATGCTCTTAAGGAAGAGGAAGAGACGAAAACGTATTGCTGAGAGGGAGCGTAGCGAGAAAATTGAGAGAGGTG
	1	-----
ATRX ORF HAP-66D4	4561	ATAGAAATTGAAGATGCTTCACCCACCAAGTGTCCAATAACAACCAAGTTGGTTTAGATGAAGATGAAGAAACCAAAGA
	1	-----
ATRX ORF HAP-66D4	4641	ACCTTTAGTGCAGGTTCATAGAAATATGGTTATCAAATTGAAACCCCATCAAGTAGATGGTTAGTTAGTGGGATT
	1	-----
ATRX ORF HAP-66D4	4721	GCTGCTGTGAGTCGTGAAAAAAACAAAGAAATCTCCAGGTTCAAGGATGCTTGTGCCCCACTGTATGGGCCTTGGTAAG
	1	-----
ATRX ORF HAP-66D4	4801	ACTTACAGGTGTAAGTTCTTCATACAGTTTGTGACAAACTGGATTCAGCACGGCGTAGTGGTTGTCC
	1	-----
ATRX ORF HAP-66D4	4881	TCTTAATACTGCTTGAATTGGATGAATGAATTGAGAAGTGGCAAGAGGGATTAAAGATGATGAGAAGCTTGAGGTT
	1	-----
ATRX ORF HAP-66D4	4961	CTGAATTAGCAACTGTGAAACGTCCTCAGGAGAGAACGCTACATGCTGCAGAGGTGGCAAGAAAGATGGTGTGTTATGATC
	1	-----
ATRX ORF HAP-66D4	5041	ATAGGCTATGAGATGTATAGAAATCTTGCTCAAGGAAGGAATGTGAAGAGTCGAAACTTAAAGAAATTAAACAAAGC
	1	-----
ATRX ORF HAP-66D4	5121	TTTGGTTGATCCAGGCCCTGATTGTTGTGATGAAGGCCATATTCTAAAAATGAAGCATCTGCTGTTCTAAAG
	1	-----
ATRX ORF HAP-66D4	5201	CTATGAATTCTATACGATCAAGGAGGAGGATTATTTAACAGGAACACCACTTCAAAATAACCTAATTGAGTATCATG
	1	-----
ATRX ORF HAP-66D4	5281	ATGGTTAATTCTACGAAAGGAAATTACTTGGATCCATTAGGAGTTCAAGGAATAGATTATAAAATCCAATTCAAAATGG
	1	-----
ATRX ORF HAP-66D4	5361	TCAGTGTGCAAGATTCTACCATGGTAGATGTCAGAGTGTGATGCAAAACGTGCTCACATTCTCTATGAGATGTTAGCTGGAT
	45	TCAGTGTGCAAGATTCTACCATGGTAGATGTCAGAGTGTGATGCAAAACGTGCTCACATTCTCTATGAGATGTTAGCTGGAT
ATRX ORF HAP-66D4	5441	GTGTTCAAGAGGAAGATTATACGATTAACAAAATTCTGCCTCCAAAACACGAATATGTGTTAGCTGTGAGAATGACT
	125	GTGTTCAAGAGGAAGATTATACGATTAACAAAATTCTGCCTCCAAAACACGAATATGTGTTAGCTGTGAGAATGACT
ATRX ORF HAP-66D4	5521	TCTATTCAAGTGCAGCTCTATCACTACTACTAGTCCTAACAGGTGTGGGCAATAATAGTGAAGGTGGAAAGAGGAAA
	205	TCTATTCAAGTGCAGCTCTATCACTACTACTAGTCCTAACAGGTGTGGGCAATAATAGTGAAGGTGGAAAGAGGAAA

ATRX ORF HAP-66D4	5601	GGCAGGTGCAAAGCTTTCCAAGATTTCAGATGTTAAGTAGAATATGGACTCATCCTGGTGGCACTAGACTACA
	285	<b>GGCAGGTGCA</b> -----
ATRX ORF HAP-66D4	5681	TTAGCAAAGAAAATAAGGGTTATTTGATGAAGACAGTATGGATGAATTATAGCCTCAGATTCTGATGAAACCTCCATG
	294	-----
ATRX ORF HAP-66D4	5761	AGTTAACGCTCCGATGATTATACAAAAAAGAAGAAAAAGGGAAAAAGGGAAAAAGAGATAGTAGCTCAAGTGGAAAGTGG
	294	-----
ATRX ORF HAP-66D4	5841	CAGTGACAATGATGTTGAAGTGTAAAGGCTGGAATTCAAGATCTCGGGGAGGTGGTAAGGAAATGTGGATGAAACAG
	294	-----
ATRX ORF HAP-66D4	5921	GAAACAATCCTCTGTTCTTAAACTGGAAGAAAGTAAAGCTACTTCTTCTAATCCAAGCAGCCCAGCTCCAGAC
	294	-----
ATRX ORF HAP-66D4	6001	TGGTACAAAGATTTGTTACAGATGCTGATGCTGAGGTTTAGAGCATTGAGGAAATGGTACTTCTCTTGAAATTCT
	294	-----
ATRX ORF HAP-66D4	6081	TCGAATGGCAGAGGAATTGGGATAAAGTCCTGTTTCAGCCAGTCCCATATCTCTGGACTTGATTGAAGATTTC
	294	-----
ATRX ORF HAP-66D4	6161	TTGAATTAGCTAGTAGGGAGAACAGAACAGATAAAAGATAAAACCCCTATTATAAGGTGAGGGAAAGTGGCTCGAAC
	294	-----
ATRX ORF HAP-66D4	6241	ATTGACTATTACCGTTAGATGGTCCACTACTGCACAGTCAGGAAGAAGTGGCTGAAGAATTAAATGATGAAACTAA
	294	-----
ATRX ORF HAP-66D4	6321	TGTGAGAGGACGATTATTATCATTCTACTAAAGCAGGATCTCTAGGAATTAAATCTGGTAGCTGCTAATCGAGTAATTA
	294	-----
ATRX ORF HAP-66D4	6401	TATTCGACGCTTCTGGAATCCATCTTATGACATCCAGAGTATATTAGCTTGGACAAACTAACGCTGTT
	294	-----
ATRX ORF HAP-66D4	6481	TATGTATATAGGTTCTAGCTCAGGGAACCATGGAAGATAAGATTATGATCGCAAGTAACAGCAGTCAGTGTCTT
	294	-----
ATRX ORF HAP-66D4	6561	TCGAGTTGTTGATCAGCAGCAGGTGGAGCGTCATTTACTATGAATGAGCTTACTGAACCTTATACTTTGAGCCAGACT
	294	-----
ATRX ORF HAP-66D4	6641	TATTAGATGACCTAATTCAAGAAAAGAAGAACAGAGGGATACTCCCATGCTGCCAAAGGATACCATACGGCTGAGCTC
	294	-----
ATRX ORF HAP-66D4	6721	CTTCAGATACATAAGAACACATGTTAGGATACCATGAACATGATTCTCTTGGACCACAAAGAAGAACAGTTGAC
	294	-----
ATRX ORF HAP-66D4	6801	TGAAGAAGAAAGAAAAGCAGCTGGGCTGAGTATGAAGCAGAGAACAGGTACTGACCATGCGTTCAACATACCAACTG
	294	-----
ATRX ORF HAP-66D4	6881	GGACCAATTACCCCTGTCAGTTCAACTCTCAAACCTCTATATTCCCTTCAATTGGGAGCCCTGTCAGCAATGAGT
	294	-----
ATRX ORF HAP-66D4	6961	AATCAACAGCTGGAGGACCTCATTAATCAAGGAAGAGAAAAGTTGAGAACAGCAACAAACAGTGTGACAGCAGTGAGGAT
	294	-----
ATRX ORF HAP-66D4	7041	TCAACCTTGTGAGGATATAATTTCAGCTGTATGGAAGGAAACATGAATCTCTCAGAGGCCAAGTACAGCGTTAGCAT
	294	-----
ATRX ORF HAP-66D4	7121	TAAGTAGACAAGCCAGCCAGGAGCTGATGTTAACGAAGAGAACAGCAATCTACAATGATGTATTGACAAAACAACAGATG
	294	-----
ATRX ORF HAP-66D4	7201	TTAACCTGCTGTTCAAGCAATACTTATGAAACAGAAGGCTCCAGCAGCAGTACAATCAGCAGCAACAGCAACAAATGAC
	294	-----
ATRX ORF HAP-66D4	7281	TTATCAACAAGAACACTGGTCACCTCATGATGCCAAGGCCAAATTGATCATGAACTCCTCTAACACCAGCAGCAG
	294	-----
ATRX ORF HAP-66D4	7361	TTGATATGAGAGGAATGTATCAGCCAGTGGCTGGTGGTATGCAGCCACCACATTACAGCGTGCACCACCCCAATGAGA
	294	-----
ATRX ORF HAP-66D4	7441	AGCAAAATCCAGGACCTTCCAAGGGAAATCAATGTGA
	294	-----

## b) AS fragment No. 2 (TXA-1B3)

ATRX ORF	1	ATGACCGCTGAGCCCAGTGAAGCAAGTTGAATACATTGGTCAGAACGTTCATGACTTCCTGCACACTCATCAGA
TXA-1B3	1	-----
ATRX ORF	81	AGAATCTGAAGAACAAAGTTCTCCCTCACGACTTGCAATGAATCAAACACAGATAAAACTACAGTGGTTCTGGAAGTAAC
TXA-1B3	1	-----
ATRX ORF	161	CTGATATGATGGAAAACAGCAAGGAAGAGGAACTAGCTCTCAGAAAAATCCAAGTCTCAGGATCGTCACGATCAAAG
TXA-1B3	1	-----
ATRX ORF	241	AGGAAACCTCAATTGTAACAAAGTATGTAGAATCAGATGATGAAAAACCTTGGATGATGAAACTGTAATGAAGATGC
TXA-1B3	1	-----
ATRX ORF	321	GTCTAATGAAAATTCAAGAAAATGATATTACTATGCAGAGCTGCCAAAAGGTACAGTGATTGTACAGCCAGAGCCAGTGC
TXA-1B3	1	-----
ATRX ORF	401	TGAATGAAAGACAAGATGATTTAAAGGGCTGAAATTAGAAGCAGAAGTAAAATGAAAACGACTCAAACAAAGCC
TXA-1B3	1	-----
ATRX ORF	481	GGAGAAAGATGGGCTTCATGGGATTGTGAGCTGCACTGCTTGTGGACAACAGGTCAATCTTCAAAAGATTCCATT
TXA-1B3	1	-----
ATRX ORF	561	TAGACACCCATTGCAAGTTCTATTGTAAGATTGCTTAAGTATTACATGAGTGATGATATTAGCCGTGACTCAG
TXA-1B3	1	-----
ATRX ORF	641	ATGGAATGGATGAACAATGTAGGTGGTGTGGAGAGTGGAAACTTGATTGTTGACTTTGCCATAATGCTTCTGC
TXA-1B3	1	-----
ATRX ORF	721	AAGAAAATGCATTCTACGCAACCTTGGCGAAAGGAGTTGTCACATAATGGATGAAAACAACCAATGGTATTGCTACAT
TXA-1B3	1	-----
ATRX ORF	801	TTGTCACCCAGAGCCTTGTGGACTTGGCACTGCATGTAACAGCGTATTGAGAATTAGAACAGTTGTCAGCAA
TXA-1B3	1	-----
ATRX ORF	881	ATAAGAAGAAGATAAAAGTTGACAGTGAAAAGAGTAATAAAGTATATGAACATACATCCAGATTCTCAAAGAAGACT
TXA-1B3	1	-----
ATRX ORF	961	AGTTCAAATTGTAATGGAGAAGAAAAGAAATTAGATGATTCTGTTCTGGCTCTGTAACCTACTCTTATTCCGCACTAAT
TXA-1B3	1	-----
ATRX ORF	1041	TGTGCCAAAGAGATGATTAAGAAGGCAAAAAACTGATTGAGACCACAGCAACATGAACCTCCAGTTATGTTAAATT
TXA-1B3	1	-----
ATRX ORF	1121	TAAAGCAGGCAACAGATAATTGCAAAATCAGTTCTGCTACAAAATTACGTCAGCTTAAGGCTTTAAGTCTGTGTTGGCT
TXA-1B3	1	-----
ATRX ORF	1201	GATATTAAGAAGGCTCATCTGCATTGGAAGAAGACTTAAATTCCGAGTTGAGCGATGGATGCTGTAACAAAGAGAA
TXA-1B3	1	-----
ATRX ORF	1281	AAATACCAAAGAGCATAAAGTCATAGATGCTAAGTTGAAACAAAAGCAGAAAAGGAGAAAACCTTGTGCTTGGAAA
TXA-1B3	1	-----
ATRX ORF	1361	AGAAGGATATTCAAAGTCAGAGCTAAACTTCAAGAAAACAGGTAGATAGTGACCACATGCATCAGAATGTTCAAACA
TXA-1B3	1	-----
ATRX ORF	1441	GAGGAACAAAGAACAAATAAAAGYACCGGTGGTAACATAAGAAAATCTGATAGAAAAGAGAACCTCAATATGAACCTGC
TXA-1B3	1	-----
ATRX ORF	1521	CAACACTCTGAAAGATTTAGACATGGATATTGTTGCTGTTCTCAGTTCCAGAACAGACATTGAGAATCTTGAGA
TXA-1B3	1	-----
ATRX ORF	1601	CTGCTATGGAAGTTCAGAGTTCACTGATCATCAAGGGATGGCAGCAGTGGAACTGAACAAGAAGTGGAGAGTTCATCT
TXA-1B3	1	-----
ATRX ORF	1681	GTAAAATTAAATATTCTCAAAAGACAACAGAGGAGGTATAAATCAAACACTACAGCTAAAGTAACAAAAGAATTATA
TXA-1B3	1	-----
ATRX ORF	1761	TGTTAAACTCACTCCTGTTCCCTCTAATTCCCAATTAAAGGTGCTGATTGTCAGGAAGTTCCACAAGATAAAGATG

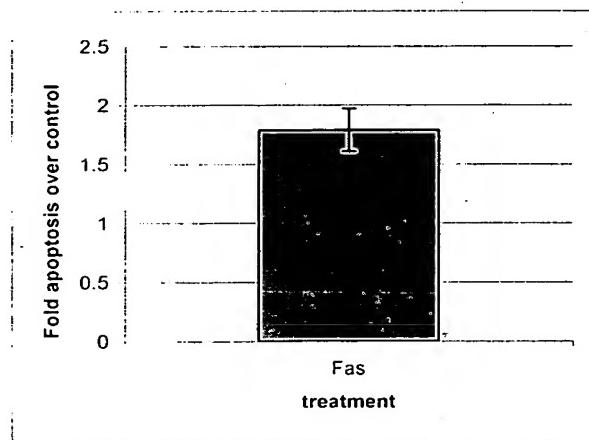
TXA-1B3	1	-----
ATRX ORF	1841	GCTATAAAAGTTGGTCTGAACCCCAAGTTAGAGAAATGTGGACTGGACAGGAAAACAGTGATAATGAGCATTGGTT
TXA-1B3	1	-----
ATRX ORF	1921	GAAAATGAAGTTCATTAAGTAGAGGAATCTGATCTCGGAGATCCCACGTCAAAGACTACACCCCTGAGGCAGCC
TXA-1B3	1	-----
ATRX ORF	2001	GACAGAACTAACCTGTAACATCTAACATTAGATGAAGAATGTAATGAAACAGTTAAGGAGAAACAAACTATCAGTC
TXA-1B3	1	-----
ATRX ORF	2081	CAGTGAGAAAAAAGGATAAGCGTAATTCTCTGACAGTGCTATAGATAATCCTAACGCCAATAAATTGCCAAATCTAAG
TXA-1B3	1	-----
ATRX ORF	2161	CAATCAGAGACTGTGGATCAAATTAGATCTGATGAAATGCTAGCAATCCTCAAAGGGTGAGCAGGATGAGTCACAG
TXA-1B3	1	-----
ATRX ORF	2241	TTCTTCTTCAGATACTGATATTAATGAAATTACATACAAACCATAAGACTTTGTATGATTAAAGACTCAGGCGGGAAAG
TXA-1B3	1	-----
ATRX ORF	2321	ATGATAAAGGAAAAAGGAAACGAAAAAGTTCTACATCTGGCTCAGATTTGATACTAAAAAGGGCAAATCAGCTAAGAGC
TXA-1B3	1	-----
ATRX ORF	2401	TCTATAATTCTAAAAGAAACGACAACCCAGTCTGAGTCTCTAATTGACTCAGAATTAGAAAAAGAGATAAAGAG
TXA-1B3	1	-----
ATRX ORF	2481	CATGAGTAAAATTGGTCTGCCAGAACCCACCAAAAAAGAATTCCAATACAAAAGATTGACTCTCTGAAGATGAGA
TXA-1B3	1	-----
ATRX ORF	2561	AACACAGCAAAAAGGAATGGATAATCAAGGGCACAAAATTGAAGACCTCACAAGAAGGATCATCTGATGATGCTGAA
TXA-1B3	1	-----
ATRX ORF	2641	AGAAAACAAGAGAGAGACTTTCTTCAGCAGAAGGCACAGTTGATAAAGACACGACCATCATGGAATTAAGAGATCG
TXA-1B3	1	-----
ATRX ORF	2721	ACTCCCTAAGAACGCAGCAAGCAAGTGCTTCACTGATGGTGTGATAAGCTTCTGGGAAAGAGCAGAGTTTACTCTT
TXA-1B3	1	-----
ATRX ORF	2801	TGGAAGTTAGAAAAGTTGCTGAAACTAAAGAAAAGAGCAAGCATCTCAAACCAAAACATGAAAAAGTACAGGATGGC
TXA-1B3	1	-----
ATRX ORF	2881	TTATCTGATATTGCAGAGAAATTCTAAAGAAAAGACCAGAGCGATGAAACTCTGTAAGATGATAAAAAGCAGAGCAAAA
TXA-1B3	1	-----
ATRX ORF	2961	GGGAACCTGAAAGAAAAAGAAACCTTCAGACTTTAAGAAAAAGTAATTAAATGAAACACAGTATGAAATCTCATCTG
TXA-1B3	1	-----
ATRX ORF	3041	ATGGCACTGAAAAGTTACCTGACCGAGAAGAAATTGTCATTTCTAACGGCATAAAACAAATTAGAATGAAACAACT
TXA-1B3	1	-----
ATRX ORF	3121	GATGGAGAAAAGAAAAGTAAAAAAATAAGAGATAAAACTCTAAAAAGAGGATGAATTATGCTGATTATGCTGAGAAGTC
TXA-1B3	1	-----
ATRX ORF	3201	AACAGGGAAAGGAGATAGTTGACTCTTCAGAGGATAAAAGAGTAAGAATGGACATATGGTAGAGAGAAGAAAAGGT
TXA-1B3	1	-----
ATRX ORF	3281	GCAAGTTGCTGGAAAGAGTTCAAGGAAGAGACAAGATTGCTCATCTGATACTGAGAAATATTCCATGAAAGAAGAT
TXA-1B3	1	-----
ATRX ORF	3361	GGTTGTAACCTCTGATAAGAGACTGAAAAGAAATAGAATTGAGGGAAAGAAGAAATTAAAGTTCAAAGAGAAATACTAA
TXA-1B3	1	-----
ATRX ORF	3441	GGAAATACAAAGTGGCTCATCATCTGATGCTGAGGAAGAAACTCCCTAACGAAACAGCAACTAAAGGAAGCAAGCAACTTCAT
TXA-1B3	1	-----
ATRX ORF	3521	CTAAAAAGAAGGCAGTCATTGTCAGGGAGAAAAAGAGAAACTCCCTAACGAAACAGCAACTAAAGGAAGCAAGCTGACATT
TXA-1B3	1	-----
ATRX ORF	3601	ACATCCTCATCTCTGATATAGAAGATGATGATCAGAATTCTATAGGTGAGGGAAAGCAGCGATGAAACAGAAAATTAA
TXA-1B3	1	-----
ATRX ORF	3681	GCCTGTCACTGAAAATTAGTGTGCTTCACATCTGGATTGCAATCTCAGGAGATGAAGCCTTATCTAAATCAG
TXA-1B3	1	-----

ATRX ORF	3761	TGCCTGTCACAGTGGATGATGATGACGACAATGATCCTGAGAATAGAATTGCCAAGAAAGATGCTTTAGAAGAAATT
TXA-1B3	1	-----
ATRX ORF	3841	AAAGCCAATCTTCCTCTGATGAGGATGGATCTCAGATGATGAGCCAGAAGAAGGAAAAAGAACTGGAAAACAAAA
TXA-1B3	1	-----
ATRX ORF	3921	TGAAGAAAACCCAGGAGATGAGGAAGCAAAAATCAAGTCATTCTGAATCAGATTCTGAAGAATCTAAGAAC
TXA-1B3	1	-----
ATRX ORF	4001	CAAGATACAGACATAGGCTTTGCGGCACAAAATTGACTGTGAGTGACGGAGAATCTGGAGAAGAAAAAGACAAAGCCT
TXA-1B3	1	-----
ATRX ORF	4081	AAAGAGCATAAAGAAGTCAAAGGCAGAACAGAAAGGAGCAGTGAAGATTCTGAGATTCTGAGGAAATC
TXA-1B3	1	-----
ATRX ORF	4161	AGGAGTTAGTGAAGAAGTTACTGAATCCGAAAGATGAACAGCGGCCAGAACAAAGGCTGCAAAGAAAGCAGAGTTGAAG
TXA-1B3	1	-----
ATRX ORF	4241	AAAATCAGCGGAGCTATAAACAGAAAAGAAAAGGCGACGTATTAGGTTCAAGAAGATTCCAGTGAAAACAAGAGT
TXA-1B3	1	-----
ATRX ORF	4321	AATTCTGAGGAAGAAGAGGAGGAAAAGAAGAGGAGGAGGAAGAGGAGGAGGAGGAAGAGGAGGAGGAAGATGAAA
TXA-1B3	1	-----
ATRX ORF	4401	TGATGATTCCAAGTCTCCTGGAAAAGGCAGAAAGAAAATTGGAAGATTCTAAAGATGATAACTGAGAACAGAAACAC
TXA-1B3	1	-----
ATRX ORF	4481	AAAATGCTCTTAAGGAAGAGGAAGAGAGACGAAAACGTATTGCTGAGAGGGAGCGTGAGCGAGAAAATTGAGAGAGGTG
TXA-1B3	1	-----
ATRX ORF	4561	ATAGAAAATTGAAGATGCTTCACCCACCAAGTGTCCAATAACAACCAAGTTGGTTTAGATGAAGATGAAGAAACCAAAGA
TXA-1B3	1	-----
ATRX ORF	4641	ACCTTAGTGCAGGTTCATAGAAATATGGTTATCAAATTGAAACCCCATCAAGTAGATGGTGTTCAGTTATGTGGGATT
TXA-1B3	1	-----
ATRX ORF	4721	GCTGCTGTGAGCTGTGAAAAAAACAAAGAAATCTCAGGTTCAAGGATGCAATTGCCCCACTGTATGGCCTTGGTAAG
TXA-1B3	1	-----
ATRX ORF	4801	ACTTTACAGGTGGTAAGTTTCTTCATACAGTTCTTGTGACAAACTGGATTTCAGCACGGCGTTAGTGGTTGTCC
TXA-1B3	1	-----
ATRX ORF	4881	TCTTAATACTGCTTGAATTGGATGAATTGAGAAGTGGCAAGAGGGATTAAAGATGATGAGAAGCTTGAGGTT
TXA-1B3	1	-----
ATRX ORF	4961	CTGAATTAGCAACTGTGAAACGTCTCAGGAGAGAACGCTACATGCTGCAGAGGTGGCAAGAAGATGGGGTTATGATC
TXA-1B3	1	-----
ATRX ORF	5041	ATAGGCTATGAGATGTATAGAAATCTTGCTCAAGGAAGGAATGTGAAGAGTCGAAACTTAAAGAAATATTAACAAAGC
TXA-1B3	1	-----
ATRX ORF	5121	TTTGGTTGATCCAGGCCCTGATTGTTGTGATGAAGGCCATATTCTAAAAATGAAGCATCTGCTTTCTAAAG
TXA-1B3	1	-----
ATRX ORF	5201	CTATGAATTCTATACGATCAAGGAGGAGGATTATTTAACAGGAACACCACCTCAAAATAACCTAATTGAGTATCATTGT
TXA-1B3	1	-----
ATRX ORF	5281	ATGGTTAATTGTTCAAGGAAAATTACTTGGATCCATTAGGAGTCAGGAATAGATTATAAATCCAATTCAAATGG
TXA-1B3	1	-----
ATRX ORF	5361	TCAGTGTGCAGATTCTACCATGGTAGATGTCAGAGTGATGAAAAACGTGCTCACATTCTATGAGATGTTAGCTGGAT
TXA-1B3	1	-----
ATRX ORF	5441	GTGTTCAGAGGAAGATTACAGCATTAAACAAAATTCTGCCCTCCAAAACACGAATATGTGTTAGCTGTGAGAATGACT
TXA-1B3	1	-----
ATRX ORF	5521	TCTATTCAAGTGCAGCTCTACGACTACTTAGATCACTTAACAGGTGGCAATAATAGTGAAGGTGGAAAGAGGAAA
TXA-1B3	1	-----
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TXA-1B3	1	-----

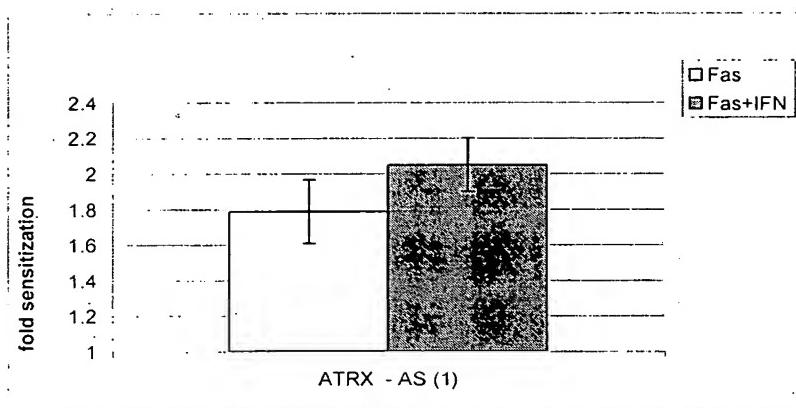
ATRX ORF TXA-1B3	5681	TTAGCAAAGAAAATAAGGTTATTTGATGAAGACAGTATGGATGAATTATAGCCTCAGATTCTGATGAAACCTCCATG 1
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ATRX ORF TXA-1B3	5841	CAGTGACAATGATGTTGAAGTGTGATTAAGGTCTGGAATTCAAGATCTCGGGAGGTGGTGAAGGAAATGTGGATGAAACAG 1
ATRX ORF TXA-1B3	5921	GAAACAATCCTCTGTTCTTAAAATGGAAGAAAGTAAAGCTACTTCTTCTAATCCAAGCAGCCCAGCTCCAGAC 1
ATRX ORF TXA-1B3	6001	TGGTACAAAGATTTGTTACAGATGCTGATGCTGAGGTTTAGAGCATTCTGGAAAATGGTACTTCTTTGAAATTCT 1
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ATRX ORF TXA-1B3	6161	TTGAATTAGCTAGTAGGGAGAAGACAGAAGATAAAGATAAACCCCTTATTATAAAGGTGAGGGAAAGTGGCTTCGAAAC 1
ATRX ORF TXA-1B3	6241	ATTGACTATTACCGTTAGATGGTCCACTACTGCACAGTCAGGAAGAACTGGGCTGAAGAATTAAATGATGAAACTAA 1
ATRX ORF TXA-1B3	6321	TGTGAGAGGAAGATTATTCATTCTACTAAAGCAGGATCTCTAGGAATTAAATCTGGTAGCTGCTAACGAGTAATTAA 1
ATRX ORF TXA-1B3	6401	TATTCGACGCTCTTGGAAATCCATCTTATGACATCCAGAGTATTCAGAGTTATCGCTTGGACAAACTAACGCCTGTT 1
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ATRX ORF TXA-1B3	6561	TCGAGTTGTTGATCAGCAGCAGGTGGAGCGTCATTTACTATGAATGAGCTTACTGAACATTATACTTTGAGCCAGACT 1
ATRX ORF TXA-1B3	6641	TATTAGATGACCCTAATTCAAGAAAAGAAGAAGAGAGGGATACTCCCATGCTGCCAAAGGATACCCACTTGAGAGCTC 1
ATRX ORF TXA-1B3	6721	CTTCAGATACTAAAGAACACATTGAGGATACCATGAACATGATTCTCTTGGACCACAAAGAAGAAGAGTTGAC 1
ATRX ORF TXA-1B3	6801	TGAAGAAGAAAGAAAAGCAGCTGGGCTGAGTATGAAGCAGAGAAGAGGTACTGACCATGCGTTAACATACCAACTG 1
ATRX ORF TXA-1B3	6881	GGACCAATTACCCCTGTCAGTTCAACTCTCAAACCTCTTATATTCTTCAATTGGGAGCCCTGTCAGCAATGAGT 1
ATRX ORF TXA-1B3	6961	AATCAACAGCTGGAGGACCTCATTAATCAAGGAAGAGAAAAGTGTAGAAGCAACAAACAGTGTGACAGCAGTGAGGAT 1
ATRX ORF TXA-1B3	7041	TCAACCTCTTGAGGATATAATTCACTGATGAGGAGAACATGAATCTCTCAGAGGCCAAGTACAGGCCTAGCAT 1
ATRX ORF TXA-1B3	7121	TAAGTAGACAAGCCAGCCAGGAGCTGATGTTAACGAAGAGCAATCTACAATGATGATGACAAAACAAGATG 1
ATRX ORF TXA-1B3	7201	<del>TTAACATGCTGTCTGCGAATCTTATGAAACAGAAGGGCTCCAGCAGCAGTACAATCAGCAGCAACNGCAACAAATGAC</del> 6 <del>TTAACATGCTGTCTGCGAATCTTATGAAACAGAAGGGCTCCAGCAGCAGTACAATCAGCAGCAACACAAATGAC</del>
ATRX ORF TXA-1B3	7281	<del>TTATCAACAAAGCAACACTGGGTCACTCATGATGCCCCAAATTGATCATGATGAACTCCTCTAATCTACCCAGCAGA</del> 86 <del>TTATCAACAAAGCAACACTGGGTCACTCATGATGCCCCAAATTGATCATGATGAACTCCTCTAATCTACCCAGCAGA</del>
ATRX ORF TXA-1B3	7361	<del>TTGATATGAGAGGAATGATCAGCCAGTGGCTGGTGTATGCAGCCACCCATTACAGCGTGCACCCACCCAAATGAGA</del> 166 <del>TTGATATGAGAGGAATGATCAGCCAGTGGCTGGTGTATGCAGCCACCCATTACAGCGTGCACCCACCCAAATGAGA</del>
ATRX ORF TXA-1B3	7441	<del>AGCAAAATCCAGGACCTTCCCAAGGGAAATCAATGATGAA</del> 246 <del>AGCAAAATCCAGGACCTTCCCAAGGGAAATCAATGATGAA</del>

**Figure 4:**  
**Validation of the anti-apoptotic effect of ATRX**

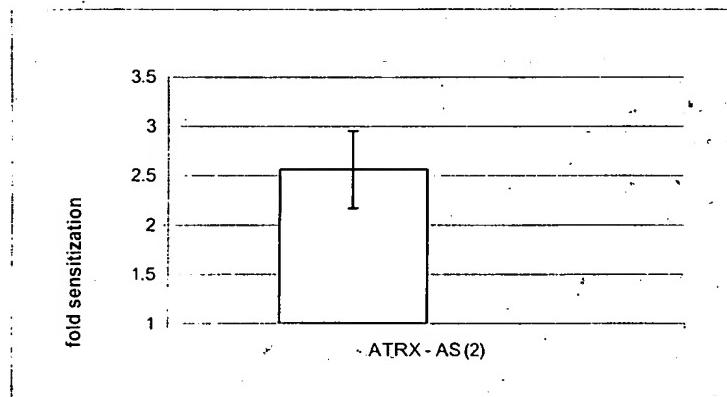
a) AS fragment No. 1 (HAP-66D4) LOF results



b)



c) AS fragment No. 2 (TXA\_1B3) LOF results



Applicants: Paz Einat et al.  
U.S. Serial No.: Not Yet Known  
Filing Date: October 30, 2003  
Title: ATRX AND USES THEREOF  
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